

# SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Acetylcholine receptor subunits

<130> Le A 34 821

<140>

<141>

<150> DE 100 42 177.6

<151> 2000-08-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 45

<212> PRT

<213> Torpedo californica

<400> 1

Asp Phe Ala Ile Val His Met Thr Lys Leu Leu Leu Asp Tyr Thr Gly  
1 5 10 15

Lys Ile Met Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile  
20 25 30

Ile Val Thr His Phe Pro Phe Asp Gln Gln Asn Cys Thr  
35 40 45

<210> 2

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1866)

<220>

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 2

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc 48  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30

gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt 144  
 Glu Arg Leu Lys Lys Leu Phe 40 Ser Gly Tyr Asn Lys 45 Trp Ser Arg

ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc 192  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60

ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca 240  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80

aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac 288  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95

ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc 336  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110

atc tgg cgg ccg gac ata gtc ctc tac aac aat gcc gac ggc aac ttc 384  
 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe  
 115 120 125

gag gta acg ctg gcg acg aag gcg act ttg aat tat acg gga cgt gtg 432  
 Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val  
 130 135 140

gag tgg cgc ccg ccg gct atc tac aag tcc tcg tgc gag atc gac gtg 480  
 Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val  
 145 150 155 160

gaa tac ttc ccg ttc gac cag cag acg tgc gtc atg aag ttc ggc tcg 528  
 Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser  
 165 170 175

tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat 576  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190

gtg gac caa ctg gac tac tgg gaa agc ggg gag tgg gtc atc att aat 624  
 Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn  
 195 200 205

gcc gtg ggc aat tac aac agc aag aaa tat gaa tgc tgc aca gag atc 672  
 Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile  
 210 215 220

tac cct gat ata act tac tcc ttc att atc cgg agg ctg ccg ctg ttc 720  
 Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe

225	230										235	240									
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act																					
Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Ile Ser Cys Leu Thr																					
	245										250	255									
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg																					
Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu																					
	260										265	270									
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca																					
Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Ile Thr																					
	275										280	285									
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat																					
Glu Ile Ile Pro Ser Thr Ser Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr																					
	290										295	300									
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc																					
Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val																					
	305										310	315									
ttt gtg ctc aac gta cac cac cgt tca cca cgt acc cac acg atg cct																					
Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro																					
	325										330	335									
gac tgg gtg agg agg gtc ttc ctt gac ata gtc cca cgt ctc ctc ttc																					
Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Thr Leu Leu Phe																					
	340										345	350									
atg aag cgg ccc tcc aca gtg aaa gac aat tgc aag aag ctt att gaa																					
Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu																					
	355										360	365									
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gac																					
Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp																					
	370										375	380									
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat																					
Met Glu Pro Asn Phe Thr Thr Ser Ser Pro Ser Pro Ser Pro Gln Ser Asn																					
	385										390	395									
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc																					
Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala																					
	405										410	415									
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct																					
Lys Pro Met Cys Lys Ser Pro Ser Ser Gly Gln Tyr Ser Met Leu His Pro																					
	420										425	430									
gag ccc cca cag gtg acg tgt tcc tct cgg aag ccc tcc tgc cac ccc																					
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro																					
	435										440	445									

ctg	agt	gac	acc	cag	acc	aca	tct	atc	tca	aaa	ggc	aga	tcg	ctc	agt	1392
Leu	Ser	Asp	Thr	Gln	Thr	Thr	Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser	
	450					455					460					
ggt	cag	cag	atg	tac	agc	ccc	aat	aag	aca	gag	gaa	ggg	agc	atc	cgc	1440
Val	Gln	Gln	Met	Tyr	Ser	Pro	Asn	Lys	Thr	Glu	Gly	Ser	Ile	Arg	480	
	465				470				475							
tgt	agg	tcc	cga	agc	atc	cag	tac	tgt	tac	ctg	cag	gag	gac	tct	tcc	1488
Cys	Arg	Ser	Arg	Ser	Ile	Gln	Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser	
				485					490					495		
cag	acc	aat	ggc	cac	tct	agt	gcc	tct	cca	gcg	tcg	cag	cgc	tgc	cac	1536
Gln	Thr	Asn	Gly	His	Ser	Ser	Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His	
			500					505					510			
ctc	aat	gaa	gag	cag	ccc	cag	cac	aag	ccc	cac	cag	tgc	aag	tgt	aag	1584
Leu	Asn	Glu	Glu	Gln	Pro	Gln	His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys	
			515				520					525				
tgc	aga	aag	gga	gag	gca	gct	ggc	aca	ccg	act	caa	gga	agc	aag	agc	1632
Cys	Arg	Lys	Gly	Glu	Ala	Ala	Gly	Thr	Pro	Thr	Gln	Gly	Ser	Lys	Ser	
			530			535					540					
cac	agc	aac	aaa	gga	gaa	cac	ctc	gtg	ctg	atg	tcc	cca	gcc	ctg	aag	1680
His	Ser	Asn	Lys	Gly	Glu	His	Leu	Val	Leu	Met	Ser	Pro	Ala	Leu	Lys	
	545				550				555					560		
ctg	gcg	gtg	gaa	ggg	gtc	cac	tac	att	gca	gac	cac	ctg	cga	gca	gaa	1728
Leu	Ala	Val	Glu	Gly	Val	His	Tyr	Ile	Ala	Asp	His	Leu	Arg	Ala	Glu	
				565					570					575		
gat	gca	gat	ttc	tca	gtg	aag	gaa	gac	tgg	aag	tac	gta	gca	atg	gtc	1776
Asp	Ala	Asp	Phe	Ser	Val	Lys	Glu	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val	
			580					585				590				
att	gac	cgg	atc	ttt	ctc	tgg	atg	ttc	atc	atc	gtg	tgt	ttg	ctg	ggg	1824
Ile	Asp	Arg	Ile	Phe	Leu	Trp	Met	Phe	Ile	Ile	Val	Cys	Leu	Leu	Gly	
			595				600					605				
acc	gtt	ggg	ctc	ttc	ctc	ccg	ccg	tgg	ctg	gca	gga	atg	atc	taa		1869
Thr	Val	Gly	Leu	Phe	Leu	Pro	Pro	Trp	Leu	Ala	Gly	Met	Ile			
	610					615					620					

<210> 3  
 <211> 622  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 3

Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30  
 Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110  
 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe  
 115 120 125  
 Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val  
 130 135 140  
 Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val  
 145 150 155 160  
 Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser  
 165 170 175  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190  
 Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn  
 195 200 205  
 Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile  
 210 215 220  
 Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe  
 225 230 235 240  
 Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr  
 245 250 255  
 Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu  
 260 265 270  
 Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Ile Thr  
 275 280 285

Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr  
 290 295 300  
 Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val  
 305 310 315 320  
 Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro  
 325 330 335  
 Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe  
 340 345 350  
 Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu  
 355 360 365  
 Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp  
 370 375 380  
 Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn  
 385 390 395 400  
 Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala  
 405 410 415  
 Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro  
 420 425 430  
 Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro  
 435 440 445  
 Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser  
 450 455 460  
 Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg  
 465 470 475 480  
 Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser  
 485 490 495  
 Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His  
 500 505 510  
 Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys  
 515 520 525  
 Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser  
 530 535 540  
 His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys  
 545 550 555 560  
 Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu  
 565 570 575

Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val  
580 585 590

Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
595 600 605

Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
610 615 620

<210> 4  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 4  
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<210> 5  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 5  
gtcatatgtc cacgagccga ac 22

<210> 6  
<211> 1896  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(1893)

<220>  
<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 6  
atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc 48  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag	96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	
20 25 30	
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
Glu Arg Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	
35 40 45	
ccc gtc gcc aac att tgc gat gtg gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
115 120 125	
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att	432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile	
130 135 140	
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt	480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val	
145 150 155 160	
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct	528
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
cgc ggg acc aac gtg gtg gag ctg ggc gtg gac caa ctg gac tac tgg	624
Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp	
195 200 205	
gaa agc ggg gag tgg gtc atc att aat gcc gtg ggc aat tac aac agc	672
Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser	
210 215 220	
aag aaa tat gaa tgc tgc aca gag atc tac cct gat ata act tac tcc	720
Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser	



225	230										235	240									
ttc att atc cgg agg ctg ccg ctg ttc tac aca atc aat ttg atc att 768 Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr 250 Thr Ile Asn Leu Ile Ile 255																					
ccc tgc ctg ctt atc tcc tgc ttg act gtc ctg gtc ttc tac cta ccc 816 Pro Cys Leu Leu Ile Ser Cys Leu Thr 265 Val Leu Val Phe Tyr 270 Leu Pro																					
tct gag tgc gga gag aag ata acc ttg tgc atc tct gtg ctg cta tcc 864 Ser Glu Cys Gly Glu Lys Ile Thr 280 Leu Cys Ile Ser Val Leu Leu Ser 285																					
ctc acg gtg ttc ctg ctg ctc atc aca gag atc atc cct tct acc tcc 912 Leu Thr Val Phe Leu Leu Leu Ile Thr 290 Thr Glu Ile Ile Pro Ser Thr Ser 300																					
ctg gtc atc ccc ctg ata gga gag tat ctg ctc ttc acc atg ata ttt 960 Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe 305 310 315 320																					
gtc acc ttg tct atc atc atc act gtc ttt gtg ctc aac gta cac cac 1008 Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His 325 330 335																					
cgt tca cca cgt acc cac acg atg cct gac tgg gtg agg agg gtc ttc 1056 Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe 340 345 350																					
ctt gac ata gtc cca cgt ctc ctc ttc atg aag cgg ccc tcc aca gtg 1104 Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val 355 360 365																					
aaa gac aat tgc aag aag ctt att gaa tct atg cac aaa cta acc aac 1152 Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn 370 375 380																					
tca cca agg ctt tgg tct gag acc gac atg gag ccc aac ttc act acc 1200 Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr 385 390 395 400																					
tca tcc tcc ccc agc ccc cag agt aat gaa cct tca ccc aca tct tcc 1248 Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser 405 410 415																					
ttc tgt gcc cac ctt gag gag cca gcc aaa cct atg tgc aaa tcc cct 1296 Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro 420 425 430																					
tct gga cag tac tca atg ctg cac cct gag ccc cca cag gtg acg tgt 1344 Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys 435 440 445																					

tcc tct ccg aag ccc tcc tgc cac ccc ctg agt gac acc cag acc aca	1392
Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr	
450 455 460	
tct atc tca aaa ggc aga tgc ctc agt gtt cag cag atg tac agc ccc	1440
Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Met Tyr Ser Pro	
465 470 475 480	
aat aag aca gag gaa ggg agc atc cgc tgt agg tcc cga agc atc cag	1488
Asn Lys Thr Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln	
485 490 495	
tac tgt tac ctg cag gag gac tct tcc cag acc aat ggc cac tct agt	1536
Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser	
500 505 510	
gcc tct cca gcg tgc cag cgc tgc cac ctc aat gaa gag cag ccc cag	1584
Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Gln Pro Gln	
515 520 525	
cac aag ccc cac cag tgc aag tgt aag tgc aga aag gga gag gca gct	1632
His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala	
530 535 540	
ggc aca ccg act caa gga agc aag agc cac agc aac aaa gga gaa cac	1680
Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His	
545 550 555 560	
ctc gtg ctg atg tcc cca gcc ctg aag ctg gcg gtg gaa ggg gtc cac	1728
Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His	
565 570 575	
tac att gca gac cac ctg cga gca gaa gat gca gat ttc tca gtg aag	1776
Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys	
580 585 590	
gaa gac tgg aag tac gta gca atg gtc att gac cgg atc ttt ctc tgg	1824
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp	
595 600 605	
atg ttc atc atc gtg tgt ttg ctg ggg acc gtt ggg ctc ttc ctc ccg	1872
Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro	
610 615 620	
ccg tgg ctg gca gga atg atc taa	1896
Pro Trp Leu Ala Gly Met Ile	
625 630	

<210> 7

<211> 631

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified alpha

4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 7  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15  
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
20 25 30  
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
35 40 45  
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
50 55 60  
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
65 70 75 80  
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
85 90 95  
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
100 105 110  
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
115 120 125  
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
130 135 140  
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val  
145 150 155 160  
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
165 170 175  
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
180 185 190  
Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp  
195 200 205  
Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser  
210 215 220  
Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser  
225 230 235 240  
Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile  
245 250 255  
Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro  
260 265 270

Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser  
 275 280 285  
 Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser  
 290 295 300  
 Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe  
 305 310 315 320  
 Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His  
 325 330 335  
 Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe  
 340 345 350  
 Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val  
 355 360 365  
 Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn  
 370 375 380  
 Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr  
 385 390 395 400  
 Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser  
 405 410 415  
 Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro  
 420 425 430  
 Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys  
 435 440 445  
 Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr  
 450 455 460  
 Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro  
 465 470 475 480  
 Asn Lys Thr Glu Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln  
 485 490 495  
 Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser  
 500 505 510  
 Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln  
 515 520 525  
 His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala  
 530 535 540  
 Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His  
 545 550 555 560



<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 10  
atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc 48  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96  
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
20 25 30

gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt 144  
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
35 40 45

ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc 192  
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
50 55 60

ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca 240  
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
65 70 75 80

aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac 288  
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
85 90 95

ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc 336  
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
100 105 110

atc tgg agg cgc gac att gtc cta tac aac aat gct gat ggt gac ttt 384  
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
115 120 125

gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att 432  
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
130 135 140

aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt 480  
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Cys Ser Ile Asp Val  
145 150 155 160

acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct 528  
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
165 170 175

tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat 576  
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
180 185 190

gtc gac ctg tcc gag ttc tac acc tcc gtg gag tgg gac atc ctg gag 624

Val	Asp	Leu	Ser	Glu	Phe	Tyr	Thr	Ser	Val	Glu	Trp	Asp	Ile	Leu	Glu	
		195					200					205				
gtg	cca	gcc	gtc	agg	aac	gag	aag	ttc	tac	acg	tgc	tgc	gac	gag	ccc	672
Val	Pro	Ala	Val	Arg	Asn	Glu	Lys	Phe	Tyr	Thr	Cys	Cys	Asp	Glu	Pro	
		210				215					220					
tac	ctg	gac	ata	acg	ttt	aac	ttc	att	atc	cgg	agg	ctg	ccg	ctg	ttc	720
Tyr	Leu	Asp	Ile	Thr	Phe	Asn	Phe	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	
		225			230					235					240	
tac	aca	atc	aat	ttg	atc	att	ccc	tgc	ctg	ctt	atc	tcc	tgc	ttg	act	768
Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	
				245					250					255		
gtc	ctg	gtc	ttc	tac	cta	ccc	tct	gag	tgc	gga	gag	aag	ata	acc	ttg	816
Val	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	
			260					265					270			
tgc	atc	tct	gtg	ctg	cta	tcc	ctc	acg	gtg	ttc	ctg	ctg	ctc	atc	aca	864
Cys	Ile	Ser	Val	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	
		275					280					285				
gag	atc	atc	cct	tct	acc	tcc	ctg	gtc	atc	ccc	ctg	ata	gga	gag	tat	912
Glu	Ile	Ile	Pro	Ser	Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	
		290					295				300					
ctg	ctc	ttc	acc	atg	ata	ttt	gtc	acc	ttg	tct	atc	atc	atc	act	gtc	960
Leu	Leu	Phe	Thr	Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Ile	Ile	Thr	Val	
		305			310					315					320	
ttt	gtg	ctc	aac	gta	cac	cac	cgt	tca	cca	cgt	acc	cac	acg	atg	cct	1008
Phe	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	
				325					330					335		
gac	tgg	gtg	agg	agg	gtc	ttc	ctt	gac	ata	gtc	cca	cgt	ctc	ctc	ttc	1056
Asp	Trp	Val	Arg	Arg	Val	Phe	Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe	
			340					345					350			
atg	aag	cgg	ccc	tcc	aca	gtg	aaa	gac	aat	tgc	aag	aag	ctt	att	gaa	1104
Met	Lys	Arg	Pro	Ser	Thr	Val	Asn	Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	
		355					360					365				
tct	atg	cac	aaa	cta	acc	aac	tca	cca	agg	ctt	tgg	tct	gag	acc	gac	1152
Ser	Met	His	Lys	Leu	Thr	Asn	Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp	
		370				375					380					
atg	gag	ccc	aac	ttc	act	acc	tca	tcc	tcc	ccc	agc	ccc	cag	agt	aat	1200
Met	Glu	Pro	Asn	Phe	Thr	Thr	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	
		385			390					395					400	
gaa	cct	tca	ccc	aca	tct	tcc	ttc	tgt	gcc	cac	ctt	gag	gag	cca	gcc	1248
Glu	Pro	Ser	Pro	Thr	Ser	Ser	Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	
				405					410					415		

aaa cct atg tgc	aaa tcc cct tct	gga cag tac tca	atg ctg cac cct	1296
Lys Pro Met Cys	Lys Ser Pro Ser	Gly Gln Tyr Ser	Leu His Pro	
420		425	430	
gag ccc cca cag	gtg acg tgt tcc	tct ccg aag ccc	tcc tgc cac ccc	1344
Glu Pro Pro Gln	Val Thr Cys Ser	Ser Pro Lys Pro	Ser Cys His Pro	
435	440	445		
ctg agt gac acc	cag acc aca tct	atc tca aaa ggc	aga tcg ctc agt	1392
Leu Ser Asp Thr	Gln Thr Thr Ser	Ile Ser Lys Gly	Arg Ser Leu Ser	
450	455	460		
gtt cag cag atg	tac agc ccc aat	aag aca gag gaa	ggg agc atc cgc	1440
Val Gln Gln Met	Tyr Ser Pro Asn	Lys Thr Glu Glu	Gly Ser Ile Arg	
465	470	475	480	
tgt agg tcc cga	agc atc cag tac	tgt tac ctg cag	gag gac tct tcc	1488
Cys Arg Ser Arg	Ser Ile Gln Tyr	Cys Tyr Leu Gln	Glu Asp Ser Ser	
485		490	495	
cag acc aat ggc	cac tct agt gcc	tct cca gcg tcg	cag cgc tgc cac	1536
Gln Thr Asn Gly	His Ser Ser Ala	Ser Pro Ala Ser	Gln Arg Cys His	
500		505	510	
ctc aat gaa gag	cag ccc cag cac	aag ccc cac cag	tgc aag tgt aag	1584
Leu Asn Glu Glu	Gln Gln Pro Gln	His Pro His Gln	Cys Lys Cys Lys	
515	520	525		
tgc aga aag gga	gag gca gct ggc	aca ccg act caa	gga agc aag agc	1632
Cys Arg Lys Gly	Glu Ala Ala Gly	Thr Pro Thr Gln	Gly Ser Lys Ser	
530	535	540		
cac agc aac aaa	gga gaa cac ctc	gtg ctg atg tcc	cca gcc ctg aag	1680
His Ser Asn Lys	Gly Glu His Leu	Val Leu Met Ser	Pro Ala Leu Lys	
545	550	555	560	
ctg gcg gtg gaa	ggg gtc cac tac	att gca gac cac	ctg cga gca gaa	1728
Leu Ala Val Glu	Gly Val His Tyr	Ile Ala Asp His	Leu Arg Ala Glu	
565		570	575	
gat gca gat ttc	tca gtg aag gaa	gac tgg aag tac	gta gca atg gtc	1776
Asp Ala Asp Phe	Ser Ser Val Lys	Glu Asp Trp Lys	Tyr Val Ala Met	
580		585	590	
att gac ccg atc	ttt ctc tgg atg	ttc atc atc gtg	tgt ttg ctg ggg	1824
Ile Asp Arg Ile	Phe Leu Trp Met	Phe Ile Ile Val	Cys Leu Leu Gly	
595	600	605		
acc gtt ggg ctc	ttc ctc ccg tgg	ctg gca gga atg	atc taa	1869
Thr Val Gly Leu	Phe Leu Pro Pro	Trp Leu Ala Gly	Met Ile	
610	615	620		



<210> 11  
 <211> 622  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 11  
 Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30  
 Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110  
 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
 115 120 125  
 Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
 130 135 140  
 Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val  
 145 150 155 160  
 Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
 165 170 175  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190  
 Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu  
 195 200 205  
 Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro  
 210 215 220  
 Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe  
 225 230 235 240

Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr  
245 250 255

Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu  
260 265 270

Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr  
275 280 285

Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr  
290 295 300

Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val  
305 310 315 320

Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro  
325 330 335

Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe  
340 345 350

Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu  
355 360 365

Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp  
370 375 380

Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn  
385 390 395 400

Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala  
405 410 415

Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro  
420 425 430

Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro  
435 440 445

Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser  
450 455 460

Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg  
465 470 475 480

Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser  
485 490 495

Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His  
500 505 510

Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys  
515 520 525

Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser  
530 535 540

His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys  
545 550 555 560

Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu  
565 570 575

Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val  
580 585 590

Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
595 600 605

Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
610 615 620

<210> 12  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
caacagcaag aaatatgaat gctgcgacga gccctacctt gatataactt tcaacttcat 60  
tatcggagg ctgcgctg 79

<210> 13  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cagcggcagc ctccggataa tgaagttgaa agttatatca aggtagggct cgtcgcagca 60  
ttcatatttc ttgctgttg 79

<210> 14  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
gaacaaaagc tggaggtcca ccgcggtggc

30

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
gccaccgcgg tggacctcca gcttttgttc

30

<210> 16  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
gcggggagtg ggatcatcta gaagtcccg cgttcgcaa cgaaaagttt tatacatgct 60  
gcgacgagcc ctacc 75

<210> 17  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
ggtagggctc gtcgcagcat gtataaaact ttctgttgcg aacggccggg acttcaatga 60  
tgacccactc cccgc